In the specification:

Replace the indicated paragraphs with the following:

On page 10, lines 3-9, delete "(http:www.ebi.ac.uk/ interpro)" and insert -- (URL located at www.ebi.ac.uk/interpro) --, such that lines 3-9 appear as follows:

The presence of identifiable domains in AMF1, as well as all other AMFX proteins, can be determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (URL located at www.ebi.ac.uk/interpro). DOMAIN results can then be collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections.

On page 13, line 46, through page 14, line 2, make the following changes:

The presence of identifiable domains in ~~AMF1~~ AMF2, as well as all other AMFX proteins, can be determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website ~~(http:www.ebi.ac.uk/ interpro)~~. DOMAIN results can then be collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections.

On page 19, lines 1-7, make the following changes:

The presence of identifiable domains in AMF3, as well as all other AMFX proteins, can be determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website ~~(http:www.ebi.ac.uk/ interpro)~~. DOMAIN results can then be collected from the Conserved Domain Database (CDD) with

Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections.

On page 23, lines 15-28, make the following changes:

The presence of identifiable domains in AMF4, as well as all other AMFX proteins, can be determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (http:www.ebi.ac.uk/ interpro). DOMAIN results can then be collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For this DOMAIN sequence alignments, fully conserved single residues are indicated by black shading "strong" semi-conserved residues are indicated by grey. The "strong" group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK, NHQK, NDEQ, QHRK, MILV, MILF, HY, FYW. AMF4 shows good homology with the consensus sequence of the trypsin-like serine protease domain (Smart|Tryp_SPc, E= 2e-21) and the trypsin domain (Pfam00089, E= 2e-14). The alignment with the trypsin-like serine protease domain (SEQ ID NO:72)(labeled "Consensus") is shown in Table 4H.

On page 29, lines 15-21, make the following changes:

The presence of identifiable domains in AMF5, as well as all other AMFX proteins, can be determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (http:www.ebi.ac.uk/ interpro). DOMAIN results can then be collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections.

On page 32, lines 14-20, make the following changes:

The presence of identifiable domains in AMF6, as well as all other AMFX proteins, can be determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (~~http:www.ebi.ac.uk/ interpro~~). DOMAIN results can then be collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections.

On page 37, lines 25-31, make the following changes:

The presence of identifiable domains in AMF7, as well as all other AMFX proteins, can be determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the Interpro website (~~http:www.ebi.ac.uk/ interpro~~). DOMAIN results can then be collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections.